(FILE 'HOME' ENTERED AT 17:12:50 ON 22 NOV 2002) FILE 'MEDLINE, CAPLUS' ENTERED AT 17:12:59 ON 22 NOV 2002 49 S CD38 (P) GENE (P) SEQUENCE L1L2 30 DUP REM L1 (19 DUPLICATES REMOVED) FILE 'STNGUIDE' ENTERED AT 17:20:25 ON 22 NOV 2002 FILE 'MEDLINE, CAPLUS' ENTERED AT 17:25:42 ON 22 NOV 2002 10 S CD38 AND (DIABETES OR IDDM OR NIDDM) AND (MUTATION? OR POLYMO  $L_3$ L47 DUP REM L3 (3 DUPLICATES REMOVED) L5 6 S L4 NOT L2 FILE 'STNGUIDE' ENTERED AT 17:27:33 ON 22 NOV 2002 FILE 'MEDLINE, CAPLUS' ENTERED AT 17:34:56 ON 22 NOV 2002 17 S CD38 AND INSULIN AND (MUTATION? OR POLYMORPHISM?) L6 L7 13 DUP REM L6 (4 DUPLICATES REMOVED) L8 6 S L7 NOT L4 FILE 'STNGUIDE' ENTERED AT 17:37:12 ON 22 NOV 2002 FILE 'MEDLINE, CAPLUS' ENTERED AT 17:39:27 ON 22 NOV 2002 267 S (MODY1 OR MODY2 OR MODY3) AND (MUTATION? OR POLYMORPHISM?) L9

171 DUP REM L9 (96 DUPLICATES REMOVED)

6 S L10 AND TYPE 1 AND TYPE 2

L10

L11

L11 ANSWER 3 OF 6 MEDLINE

AN 2001322865 MEDLINE

DN 21202573 PubMed ID: 11307309

TI Diabetes mellitus.

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SO RINSHO BYORI. JAPANESE JOURNAL OF CLINICAL PATHOLOGY, (2001 Feb) 49 (2) 161-4. Ref: 0
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CY Japan

DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW LITERATURE)

LA Japanese

FS Priority Journals

diabetes.

EM 200106

ED Entered STN: 20010611 Last Updated on STN: 20010611 Entered Medline: 20010607

AΒ Diabetes mellitus is a group of metabolic disorders characterized by hyperglycemia resulting from defects in insulin secretion, insulin action or both. Genetic factors contribute to the development of diabetes. Some forms such as the condition called maturity-onset diabetes of the young (MODY) result from mutations in a single gene. Other forms such as type 1 or type 2 diabetes are multifactorial in origin with different combinations of genes together with non-genetic factors contributing to the development of hyperglycemia. MODY has been a good model for studying the genetics and pathophysiology of diabetes. This form of diabetes can result from mutations in at least seven different genes: hepatocyte nuclear factor(HNF)-4 alpha/ MODY1, glucokinase/MODY2, HNF-1 alpha/MODY3, insulin promoter factor(IPF-1)/MODY4, HNF-1 beta/MODY5, NeuroD1/MODY6 and Islet(Isl)-1/MODY7. Mutations in HNF-1 alpha/MODY3 are the most common cause of MODY in Japanese identified to date accounting for about 15% of cases of MODY. Mutations in the HNF-4 alpha/ MODY1, glucokinase/MODY2, HNF-1 beta/MODY5 and Isl-1/MODY7 genes have also been found in Japanese; however, they are rare causes of MODY. Clinical studies indicate that patients with MODY are generally not obese and that all forms of MODY are characterized by pancreatic beta-cell dysfunction. Patients who have mutations in the HNF-1 beta/MODY5 gene have non-diabetic kidney dysfunction including renal cysts. Female carriers may also exhibit abnormalities in the upper vagina and uterus. Genetic approach for type 2 diabetes had done by using non-parameteric linkage analysis such as sibpair analysis which worked well and NIDDM1 and NIDDM2 have been identified to date. The responsible gene for NIDDM1 was recently identified to be Calpain 10, and SNP43 in this gene could explain all of the evidence for linkage in Mexican American type 2

L2 ANSWER 10 OF 30 CAPLUS COPYRIGHT 2002 ACS

AN 2000:815089 CAPLUS

DN 133:359765

TI Diabetes risk factor detection with CD38 gene mutations

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PA BML Inc., Japan

SO Jpn. Kokai Tokkyo Koho, 19 pp. CODEN: JKXXAF

DT Patent

LA Japanese

FAN.CNT 1

PATENT NO. KIND DATE APPLICATION NO. DATE

JP 2000316578 A2 20001121 JP 1999-131955 19990512

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AB Assessment of diabetes risk factors by detecting mutations in gene coding for type II transmembrane glycoprotein CD38 (ADP-ribosyl cyclase/cyclic ADP-ribose hydrolase), is disclosed. Polymorphism was obsd. in the exon 3 and 4 of CD38 gene from peripheral leukocytes; the corresponding point mutation of exon 3 show R140W missense mutation and that of exon 4 showed silent mutation at I 168. The allele frequency of R140W missense mutation was different between NIDDM and non-diabetic controls. Glut 2 gene mutation was also obsd. in a family with the CD38 gene mutation, indicating the involvement of CD38 gene and other genes in pathogenesis of NIDDM. DEEG (denaturing gradient gel electrophoresis), direct sequencing, and PCR-RFLP were used.